Listing of the Claims:

The following Listing of the Claims is to replace all previous Listings of the Claims.

1 - 61. (Cancelled)

62. (Currently Amended) A multiplex method of determining the identities of single nucleotides present at a group of known polymorphic sites, said method comprising:

I) providing a nucleic acid sample comprising said group of polymorphic sites;

II) separating the strands of said nucleic acid sample and re-annealing in the presence of:

a) a set of first oligonucleotide primers each comprising a 3' region that hybridizes to a sequence at a known distance upstream of a known polymorphic site of said group of polymorphic sites, each member of said set of first oligonucleotide primers comprising a common sequence tag located 5' of said 3' region, and each member of said set of first oligonucleotide primers selected such that a plurality of distinctly sized amplification ~~product~~ products is generated for each polymorphic site in said group of known polymorphic sites; and

b) a set of downstream amplification primers comprising, in 5' to 3' order:

i) a sequence tag selected from the group consisting of a tag specifically corresponding to G as the 3'-terminal nucleotide of said primer; a tag specifically corresponding to A as the 3'-terminal nucleotide of said primer; a tag specifically corresponding to T as the 3'-terminal nucleotide of said primer; and a tag specifically corresponding to C as the 3'-terminal nucleotide of said primer;

ii) a region that specifically hybridizes to a sequence adjacent to and 3' of a polymorphic site in said group of known polymorphic sites, wherein said set of downstream amplification primers comprises a subset of primers comprising a region that specifically hybridizes

adjacent to said polymorphic site for each polymorphic site in said group of known polymorphic sites; and

iii) a 3' terminal nucleotide selected from G, A, T or C, wherein said terminal nucleotide specifically corresponds to the sequence tag described in (i) on that downstream amplification primer, and wherein when said downstream amplification primer is hybridized to said sequence adjacent to and 3' of a polymorphic site, said 3' terminal nucleotide is opposite said polymorphic site;

III) contacting the annealed oligonucleotides resulting from step (II) with a nucleic acid polymerase under conditions that permit the extension of an annealed oligonucleotide such that extension products are generated, wherein the primer extension product from the first oligonucleotide primer, when separated from its complement, can serve as a template for the synthesis of the extension product of as member of the set of second oligonucleotide primers, and vice versa;

IV) repeating strand separating and contacting steps (II) and (III) two times, such that a reaction mixture comprising a population of nucleic acid molecules is generated that comprises both a sequence identical to or complementary to said first oligonucleotide and a sequence identical to or complementary to a member of said set of downstream amplification primers;

V) contacting the population generated in step (IV) with a heat-labile exonuclease under conditions permitting the degradation of non-annealed oligonucleotide primers, such that non-annealed primers are degraded;

VI) thermally inactivating said heat-labile exonuclease;

VII) subjecting said population of nucleic acid molecules to a multiplex amplification regimen, wherein said multiplex amplification regimen is performed using an upstream amplification primer comprising the common sequence tag comprised by said first oligonucleotide primer, and a set of distinguishably labeled downstream amplification primers, each member of said set of distinguishably labeled downstream amplification primers comprising a tag comprised by a member of said downstream amplification primers;

VIII) separating a plurality of distinctly sized amplification products by size and/or by charge; and

IX) detecting incorporation of at least one distinguishable label in said plurality of distinctly sized amplification products, thereby determining the identities of the nucleotides present at a member of said ~~set~~ group of known polymorphic sites, wherein the same set of distinguishably labeled primers determines the identities of the nucleotides at all members of the ~~set~~ group of ~~target~~ known polymorphic sites.

63. (Currently Amended) The method of claim 62 wherein said distinguishably labeled downstream primers comprise a fluorescent moiety. [.]

64. (Cancelled)

65. (Previously Presented) The method of claim 62 wherein said separating comprises capillary electrophoresis.

66. (Currently Amended) The method of claim 62 wherein said multiplex amplification regimen comprises at least two amplification reaction cycles, wherein each cycle comprises the steps of: 1) nucleic acid strand separation; 2) oligonucleotide primer annealing; and 3) polymerase extension of annealed primers.

67. (Currently Amended) The method of claim 66 further comprising the steps, during said multiplex amplification regimen and after at least one of said reaction cycles, of removing an aliquot of said amplification reaction, separating nucleic acid molecules by size and/or by charge, and detecting the incorporation of a said distinguishable label, wherein said detecting determines the identity of the nucleotide at said polymorphic site.

68. (Currently Amended) The method of claim 67 wherein said removing, separating and detecting are performed after each cycle in said multiplex amplification regimen.

69. (Previously Presented) The method of claim 62 wherein steps I- IX are performed in a modular apparatus comprising a thermal cycler, a sampling device, a capillary electrophoresis device and a fluorescent detector.

70. (Currently Amended) The method of claim 62 wherein said ~~first and/or said second~~ tag sequences each comprise 15 to 40 nucleotides.

71. (Original) The method of claim 62 wherein said 3' region that hybridizes to a sequence at a known distance upstream of said known polymorphic site comprises 10-30 nucleotides.

72. (Original) The method of claim 62 wherein said region that hybridizes 3' of and adjacent to said polymorphic site comprises 10-30 nucleotides.

73. (Original) The method of claim 62 wherein said set of distinguishably labeled downstream amplification primers consists of: a subset that comprises a tag sequence that specifically corresponds to the presence of A at the polymorphic site; a subset that comprises a tag sequence that specifically corresponds to the presence of C at the polymorphic site; a subset that comprises a tag sequence that specifically corresponds to the presence of G at the polymorphic site; and a subset that comprises a tag sequence that specifically corresponds to the presence of T at the polymorphic site.

74. (Withdrawn) A kit for the determination of the nucleotide present at a polymorphic site present on a nucleic acid sample, said kit comprising a set of upstream primers comprising:

a) a first primer comprising a 5'-tag sequence and 3' sequence sufficient to specifically hybridize at a known distance upstream of a known polymorphic site; and

b) a set of 4 downstream second primers, comprising in 5' to 3' order:

i) a sequence tag selected from the group consisting of a tag specifically corresponding to G as the 3'-terminal nucleotide of said primer; a tag specifically corresponding to A as the 3'-terminal nucleotide of said primer; a tag specifically

corresponding to T as the 3'-terminal nucleotide of said primer; and a tag specifically corresponding to C as the 3'-terminal nucleotide of said primer;

ii) a region that specifically hybridizes to a sequence adjacent to and 3' of a polymorphic site in said group of polymorphic sites, wherein said set of downstream amplification primers comprises a subset of primers comprising a region that specifically hybridizes adjacent to said polymorphic site for each polymorphic site in said group of polymorphic sites; and

iii) a 3' terminal nucleotide selected from G, A, T or C, wherein said terminal nucleotide specifically corresponds to the sequence tag described in (i) on that downstream amplification primer, and wherein when said downstream amplification primer is hybridized to said sequence adjacent to and 3' of a polymorphic site, said 3' terminal nucleotide is opposite said polymorphic site.

75. (Withdrawn) The kit of claim 74, further comprising a set of 5 primers lacking sequence specific for a gene in the genome of the organism being examined for polymorphisms, said primers comprising a primer comprising the tag sequence of said first primer and a set of four distinguishably labeled primers comprising the tag sequences of said set of four downstream second primers.